

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/712,629C

Source:

1Fu16

Date Processed by STIC:

5/2/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/212,629C</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide ; "Xaa" can only represent a single amino acid	



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/712,629C

DATE: 05/02/2006
TIME: 14:30:25

Input Set : A:\PTO.TS.txt
Output Set: N:\CRF4\05022006\J712629C.raw

3 <110> APPLICANT: The Procter & Gamble Company
5 <120> TITLE OF INVENTION: Composition Comprising a Mouse HRt Protein Human
6 Interacting Partner Protein Complex
8 <130> FILE REFERENCE: 9423
10 <140> CURRENT APPLICATION NUMBER: US 10/712,629C
11 <141> CURRENT FILING DATE: 2003-11-13
13 <160> NUMBER OF SEQ ID NOS: 20
15 <170> SOFTWARE: PatentIn version 3.3

ERRORED SEQUENCES

490-
W--> 527 1182 of the C-terminal portion of HR protein

523 <210> SEQ ID NO: 17) 693 (p.3)
 524 <211> LENGTH: 2079
 525 <212> TYPE: DNA ! This is a PRT sequence
 526 <213> ORGANISM: Nucleotide sequence of HRt corresponding to the amino acid residue

529 <400> SEQUENCE: 17

531 Val Thr Gln Cys Gln Ser Cys Val Gln Ala Ala Gly Glu Val Gly Val
 532 1 5 10 15
 535 Leu Thr Gly His Ser Gln Lys Ser Arg Arg Ser Pro Leu Glu Glu Lys
 536 20 25 30
 539 Gln Leu Glu Glu Asp Ser Ser Ala Thr Ser Glu Glu Gly Gly
 540 35 40 45
 543 Gly Pro Gly Pro Glu Ala Ser Leu Asn Lys Gly Leu Ala Lys His Leu
 544 50 55 60
 547 Leu Ser Gly Leu Gly Asp Arg Leu Cys Arg Leu Leu Arg Lys Glu Arg
 548 65 70 75 80
 551 Glu Ala Leu Ala Trp Ala Gln Arg Glu Gly Gln Gly Pro Ala Met Thr
 552 85 90 95
 555 Glu Asp Ser Pro Gly Ile Pro His Cys Cys Ser Arg Cys His His Gly
 556 100 105 110
 559 Leu Phe Asn Thr His Trp Arg Cys Ser His Cys Ser His Arg Leu Cys
 560 115 120 125
 563 Val Ala Cys Gly Arg Ile Ala Gly Ala Gly Lys Asn Arg Glu Lys Thr
 564 130 135 140
 567 Gly Ser Gln Glu Gln His Thr Asp Asp Cys Ala Gln Glu Ala Gly His
 568 145 150 155 160
 571 Ala Ala Cys Ser Leu Ile Leu Thr Gln Phe Val Ser Ser Gln Ala Leu
 572 165 170 175
 575 Ala Glu Leu Ser Thr Val Met His Gln Ala Trp Ala Lys Phe Asp Ile
 576 180 185 190
 579 Arg Gly His Cys Phe Cys Gln Val Asp Ala Arg Val Trp Ala Pro Gly

jp 1,3-5

Does Not Comply
Corrected Diskette Needed

invalid
(213) response
(see item 10
on Error
summary
sheet)

RAW SEQUENCE LISTING

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Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

580	195	200	205
583	Asp Gly Gly Gln Gln Lys Glu Pro Thr Glu Lys Thr Pro Pro Pro Thr Pro		
584	210	215	220
587	Gln Pro Ser Cys Asn Gly Asp Ser Asn Arg Thr Lys Asp Ile Lys Glu		
588	225	230	235
591	240		
592	Glu Thr Pro Asp Ser Thr Glu Ser Pro Ala Glu Asp Gly Ala Gly Arg		
595	245	250	255
596	Ser Pro Leu Pro Cys Pro Ser Leu Cys Glu Leu Leu Ala Ser Thr Ala		
599	260	265	270
600	Val Lys Leu Cys Leu Gly His Asp Arg Ile His Met Ala Phe Ala Pro		
603	275	280	285
604	Val Thr Pro Ala Leu Pro Ser Asp Asp Arg Ile Thr Asn Ile Leu Asp		
607	290	295	300
608	Ser Ile Ile Ala Gln Val Val Glu Arg Lys Ile Gln Glu Lys Ala Leu		
611	305	310	315
612	320		
615	Gly Pro Gly Leu Arg Ala Gly Ser Gly Leu Arg Lys Gly Leu Ser Leu		
616	325	330	335
619	Pro Leu Ser Pro Val Arg Thr Arg Leu Ser Pro Pro Gly Ala Leu Leu		
620	340	345	350
623	Trp Leu Gln Glu Pro Arg Pro Lys His Gly Phe His Leu Phe Gln Glu		
624	355	360	365
627	His Trp Arg Gln Gly Gln Pro Val Leu Val Ser Gly Ile Gln Lys Thr		
628	370	375	380
631	Leu Arg Leu Ser Leu Trp Gly Met Glu Ala Leu Gly Thr Leu Gly Gly		
632	385	390	395
635	400		
636	Gln Val Gln Ser Leu Thr Ala Leu Gly Pro Pro Gln Pro Thr Asn Leu		
639	405	410	415
643	Asp Ser Thr Ala Phe Trp Glu Gly Phe Ser His Pro Glu Thr Arg Pro		
644	420	425	430
647	Lys Leu Asp Glu Gly Ser Val Leu Leu Leu His Arg Thr Leu Gly Asp		
648	435	440	445
651	627 Leu Arg Leu Ser Leu Trp Gly Met Glu Ala Leu Gly Thr Leu Gly Gly		
652	450	455	460
655	470	475	480
656	Leu Gly Leu Thr Leu His Pro Leu Glu Pro Gln Leu Trp Ala Ala Tyr		
659	485	490	495
660	Gly Val Asn Ser His Arg Gly His Leu Gly Thr Lys Asn Leu Cys Val		
663	500	505	510
667	515	520	525
668	Pro Pro Trp Tyr Arg Ala Gln Lys Asp Phe Leu Ser Gly Leu Asp Gly		
671	530	535	540
675	Glu Gly Leu Trp Ser Pro Gly Ser Gln Thr Ser Thr Val Trp His Val		
676	545	550	555
679	560		
682	Phe Arg Ala Gln Asp Ala Gln Arg Ile Arg Arg Phe Leu Gln Met Val		
685	565	570	575
688	Cys Pro Ala Gly Ala Gly Thr Leu Glu Pro Gly Ala Pro Gly Ser Cys		
696	580	585	590

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TIME: 14:30:25

Input Set : A:\PTO.TS.txt
Output Set: N:\CRF4\05022006\J712629C.raw

679 Tyr Leu Asp Ala Gly Leu Arg Arg Leu Arg Glu Glu Trp Gly Val
680 595 600 605
683 Ser Cys Trp Thr Leu Leu Gln Ala Pro Gly Glu Ala Val Leu Val Pro
684 610 615 620
687 Ala Gly Ala Pro His Gln Val Gln Gly Leu Val Ser Thr Ile Ser Val
688 625 630 635 640
691 Thr Gln His Phe Leu Ser Pro Glu Thr Ser Ala Leu Ser Ala Gln Leu
692 645 650 655
695 Cys His Gln Gly Ala Ser Leu Pro Pro Asp His Arg Met Leu Tyr Ala
696 660 665 670
699 Gln Met Asp Arg Ala Val Phe Gln Ala Val Lys Ala Ala Val Gly Ala
700 675 680 685

E--> 703 Leu Gln Glu Ala Lys ←
704 690 (4)

707 <210> SEQ ID NO: 18 → 2079(P)

708 <211> LENGTH: 693

709 <212> TYPE: PRT ? This is a DNA sequence

710 <213> ORGANISM: C-terminal portion of hairless protein of mouse (HRt) having amino acid

acid
W-->

711 residues 490 to 1182

713 <400> SEQUENCE: 18	involved
715 gttaccaggc gccaaagctg tgcggcaggca gtcggggact gacccggccac	60
717 tcggcggatcac caccgtggc accccctggaa gagaaggcgt tgccggggatgg ggattccctct	120
719 gcccggcc aagaaggagg aggaggggctt ggcccgaaag ctgcactcaa caagggcctg	180
721 gccaaggcacc tgctgatgg ttggggggac cgactctgcc gcctgctgcg gaaggagcgg	240
723 gaggcccttg cctggcaca gcgagaaggc caggggccag ccatgacaga ggacagccca	300
725 ggcattccac attgctgcag ccgatgccac cacgactct tcaacaccca ctggagatgt	360
727 tccccactgtat gccaccggct gtgtgttagcc tgtgtcgca tagccggcgc tggaaaagaac	420
729 agggagaaaa cagggtctca ggaacagcac acagatgact gcccggatgg ggctgggcat	480
731 gtcgcctgtt ccctgatectt gacccagttt gtccctggcc aggcgcgtgc agaactgagc	540
733 actgtgatgc accaaggctg ggccaaagttt gacattcggtt ggcactgttt ctgccagggtt	600
735 gatgccccgtg tgtggccccc cggggatggg ggtcagcaga aggaaccaac agagaaaaact	660
737 cccccaactc cacaaccttc ctgcaatgga gattcaatc ggaccaagga catcaaagaa	720
739 gagaccccaag actccactga gagcccagca gaggacggtg ctggccgtc accccttcct	780
741 tgtccctctc tctgtgatgt gctagcctt actgtgtca aactctgcct gggcatgac	840
743 cggattcaca tggccttgc tccggtcacc ccagctctgc ccagtgtatgatccgcattacc	900
745 aacatcctgg acagcattat tgccgcaggta gtagaacggaa agatccaaga gaaagccctg	960
747 gggccaggcc tgcgcaggcagg gtcaggctta cgcaaggccc tgagccctcc attgtccatcca	1020
749 gtgcgaaccc ggctgtctcc tcctggagct ttgcgtgtgc tgcaggagcc taggcctaag	1080
751 catggcttcc atctcttcca ggaacactgg cggcaggccc agccctgttt agtgtcaggc	1140
753 atccagaaga cattgagact tagccctgtgg ggaatggaag cccttggac acttggtggc	1200
755 cagggtgcagt cactgactgc cttggccct ccccaagccca cgaaccttgcg cagcacagca	1260
757 ttctggggagg gattctctca tcctggagaca cgtccaaagt tagatgaggg ctctgtctcc	1320
759 ctgctacacc gaaccctggg ggataaggac gtcagcagg tgccggatcc ttgtctccagc	1380
761 ctccactcc cagaataactg tgcccaacca gggaaactca accttagcgtc ctacccccc	1440
763 ctggccctca cactgcatcc actggggccc cagctctggg cggcctatgg tgcgtggagg	1500
765 caccgtggac acctggggac caagaatcta tgccgtggagg tgcgtggagg aatcgtatca	1560
767 ctgggtgcacg ccgaggccca gtcgcctccc tggtatcgag cacagaaaga tttccctctca	1620
769 ggcctggatg gggaaaggact ctgggtctcca gggagccaga ccagcactgt gtgcgtatgt	1680
771 ttccggccccc agatgccccca gcgcatccgt cgcttctcc agatggtgcg cccagctggaa	1740

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Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

773	gcaggaacct	tggagcctgg	tgcccccaggc	agctgctact	tggatgcagg	gttgcgccga	1800
775	cggctaagag	aagagtgggg	tgtgagctgc	tggaccctgc	tgcaggctcc	tgggaagcg	1860
777	gtgctggtcc	cggctggggc	gccccatca	gtgcaggggcc	tggtgagcac	aatcagtgtc	1920
779	actcagcact	ttctgtctcc	tgagacctct	gccctctctg	ctcagctctg	ccaccaggga	1980
781	gccagcctac	cccctgacca	ccgtatgctt	tatgcccaga	tggaccggc	.tgtgttccaa	2040
E--> 783	gcagtaaagg	cggctgtggg	ggcggttacag	gaagctaaa			2079 ←

see P-5 for more info

10/7/2, 629c 5

<210> 19
<211> 30
<212> DNA
<213> Oligonucleotide primer

<400> 19
ccggaattcg tcacccagtg ccaaagctgt

30

invalid <213> response

<210> 20
<211> 49
<212> DNA
<213> Oligonucleotide primer

same error

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/712,629C

DATE: 05/02/2006

TIME: 14:30:26

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

L:527 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:

L:704 M:301 E: (44) No Sequence Data was Shown, SEQ ID:17

L:704 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2079 Found:0 SEQ:17

L:711 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:

L:783 M:301 E: (44) No Sequence Data was Shown, SEQ ID:18

L:783 M:252 E: No. of Seq. differs, <211> LENGTH:Input:693 Found:0 SEQ:18